

#10

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## SEQUENCE LISTING

<110> Fouser, Lynette  
Liu, Wei  
Deng, Bija

<120> TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING  
SAME

<130> 22058-532

<140> 10/047264

<141> 2002-01-14

<150> 60/261442

<151> 2001-01-12

<150> 60/267021

<151> 2001-02-06

<150> 60/270835

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<160> 39

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Human

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tttcacaaca ttttgcata gcaagctggg agggcactta ctggcaacag cagtgtctat 180  
tttgcagt acaaataata tggacagaga caatggaaaa ataaagaaga ctgttgggt 240  
actcaagaac tctcttgta ccttaccagt gaaacctcag acatacagga accttattac 300  
gggagggtga gggcggcctc ggctgggagc tactcagaat ggagcatgac gccgcgggttc 360  
actcccttgtt gggaaacaaa aatagatcct ccagtcata atataaccca agtcaatggc 420  
tctttgttg taattctcca tgctccaaat ttaccatata gataccaaaa ggaaaaaaaaat 480  
gtatctata aagattacta tgaactacta taccgagtt ttataattaa caattcacta 540  
gaaaaggagc aaaagggtta tgaaggggct cacagagcgg ttgaaattga agctctaaca 600  
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<213> human

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20

25

30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35                   40                   45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
 50                   55                   60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
 65                   70                   75                   80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
 85                   90                   95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
 100                105                110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
 115                120                125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
 130                135                140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
 145                150                155                160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
 165                170                175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
 180                185                190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
 195                200                205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
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Glu Arg Cys Val Glu Ile Pro  
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 gggagctact cagaatggag catgacgcgc cggttcactc cctggtgaaa aacaaaaata 480  
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ccaaatttac catatagata ccaaaaggaa aaaaatgtat ctatagaaga ttactatgaa 600  
ctactatacc gagttttat aattaacaat tcactagaaa aggagcaaaa ggttatgaa 660  
ggggctcaca gagcggttga aattgaagct ctaacaccac actccagcta ctgttagtg 720  
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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His Gln Lys Pro Ser  
65 70 75 80

Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro Gly Cys Arg Thr Leu  
85 90 95

Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
100 105 110

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
115 120 125

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
130 135 140

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
145 150 155 160

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
165 170 175

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
180 185 190

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
195 200 205

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
210 215 220

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
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Glu Arg Cys Val Glu Ile Pro  
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tttcacaaca ttttgcata gcaagctggg agggcactta ctggcaacag cagtgtctat 180  
tttgcagt acaaaaatata tggacagaga caatggaaaa ataaagaaga ctgttgggt 240  
actcaagaac tctcttgta ccttaccagt gaaacctcag acatacagga accttattac 300  
gggagggtga gggccgcctc ggctgggagc tactcagaat ggagcatgac gccgcggg 360  
actcccttgtt gggaaagagc aaaaggttt tga 393

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20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys  
115 120 125

Gly Leu  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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Asn Phe Arg Ser Val Leu Leu Trp Asp Pro Pro Gly Val Arg Lys Gly  
35 40 45

Asn Leu Ser Tyr Thr Val Gln Ala Lys Ser Ile Phe Pro Lys Gln Asn  
50 55 60

Phe Asn Asn Val Thr Thr Asn Leu Asn Val Thr Glu Cys Asp Val Ser  
65 70 75 80

Ser Leu Ser Val Tyr Gly Ala Tyr Val Leu Arg Val Arg Thr Glu Trp  
85 90 95

Glu Asp Glu His Ser Asp Trp Ala Val Val Arg Phe Lys Pro Met Ala  
100 105 110

Asp Thr Val Ile Gly Pro Pro Ser Val Asn Val Lys Ser Glu Ser Gly  
115 120 125

Thr Leu His Val Asp Phe Thr Gly Pro Ala Ala Asp Arg Glu His Asp  
130 135 140

Lys Trp Ser Leu Lys Gln Tyr Tyr Gly Ser Trp Ile Tyr Arg Ile Leu  
145 150 155 160

Tyr Trp Lys Lys Gly Ser Asn Lys Lys Val Ile His Ile Asp Thr Lys  
165 170 175

His Asn Ser Glu Ile Leu Ser Gln Leu Glu Pro Trp Thr Ile Tyr Cys  
180 185 190

Ile Gln Val Gln Gly Val Ile Pro Glu Trp Asn Lys Thr Gly Glu Arg  
195 200 205

Ser Gln Glu Leu Cys Glu Gln Thr Thr His Asn Gly Val Thr Pro Val  
210 215 220

Trp Ile Val Val Thr Val Leu Leu Gly Ser Met Leu Ala Val Ile Ile  
225 230 235 240

Ser Val Pro Val Cys Phe Phe Ala Phe Trp Tyr Leu Tyr Arg Phe Thr  
245 250 255

Lys His Val Phe Phe Pro Ser Tyr Ile Phe Pro Gln His Leu Lys Glu  
260 265 270

Phe Phe Ser Pro Val Pro Gln Glu Glu His His Phe His Asp Trp Leu  
275 280 285

Thr Val Ile Ser Glu Glu Pro Lys Ser Gln Arg Asp Glu Thr Val Glu  
290 295 300

Glu Ala Ser Arg Thr Ala Glu His His Gln Asp Ser Lys Gln Glu Ile  
305 310 315 320

Ser Asp Ser Glu Ile Leu Pro Pro Leu Glu Arg Asp Gln Thr Leu Leu  
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Thr Leu Gln Ser Gly  
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<220>  
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<400> 9  
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<210> 10  
<211> 29  
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cgccccagaa ggtccgattt cagtcgcacaa attttgcac tatggacag 180  
ggagctctt cccccagcaac aacagcatct actttgtgcac gtacaagatg tatggacaga 240  
gccaatggga agataaaagtt gactgctggg ggaccacggc gctcttctgt gacctgacca 300  
atgaaacccctt agaccatac gagctgtatt acgggagggt gatgacggcc tggctggac 360  
gccactctgc ctggaccagg acaccccgct tcactccatg gtggaaaca aaactagatc 420  
ctccggctgt gactataacc cgagtttaacg catcttgcg ggtgcttctc cgtcctccag 480  
agttgcacaa tagaaaccaa agtggaaaaa atgcatccat ggaaacttac tacggcttag 540  
tatacagagt tttcacaatc aacaattcac tagagaagga gaaaaagcc tatgaaggga 600  
ctcagagagc tggtaaattt gaaggtctga tacctcattc cagctactgc gtatggctg 660  
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Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala  
35 40 45  
  
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys  
50 55 60  
  
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr  
65 70 75 80  
  
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu  
85 90 95  
  
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala  
100 105 110  
  
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp  
115 120 125  
  
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu  
130 135 140  
  
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala  
145 150 155 160  
  
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn  
165 170 175  
  
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala  
180 185 190

Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala  
195 200 205

Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu  
210 215 220

Arg Cys Val Gln Ile Pro  
225 230

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<221> VARIANT

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<223> Wherein X is the amino acid L or F

<220>

<221> VARIANT

<222> (10)

<223> Wherein X is the amino acid L or F

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<211> 15

<212> PRT

<213> human

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<222> (11)

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<220>

<221> VARIANT

<222> (14)

<223> Wherein X is the amino acid A or P

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<210> 15

<211> 15

<212> PRT

<213> human

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<221> VARIANT  
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<220>  
<221> VARIANT  
<222> (9)  
<223> Wherein X is the amino acid M or I

<220>  
<221> VARIANT  
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<223> Wherein X is the amino acid S or R

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<210> 16  
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<213> human

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<210> 17  
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<212> PRT  
<213> human

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<223> Wherein X is the amino acid V or L

<220>  
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<223> Wherein X is the amono acid T or I

<220>  
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<223> Wherein X is the amino acid A or V

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Lys Xaa Tyr Glu Gly  
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<213> human

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<220>  
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<223> Wherein X is the amino acid I or T

<220>  
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<223> Wherein X is the amino acid M or I

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Val Ala Glu Xaa Tyr Gln Pro Met  
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<210> 19  
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<212> PRT  
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<223> Wherein X is the amino acid K or E

<220>  
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<211> 231  
<212> PRT  
<213> human

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20 25 30  
  
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45  
  
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60  
  
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80  
  
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95  
  
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110  
  
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125  
  
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140  
  
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160  
  
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175  
  
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190  
  
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205  
  
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220  
  
Glu Arg Cys Val Glu Ile Pro  
225 230

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<400> 21

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
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Thr Gly Val Ala Gly Thr Gln Ser Thr Arg Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 22

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<400> 22

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

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<400> 23  
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
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20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
       50                  55                  60  
  
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
       65                  70                  75                  80  
  
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
       85                  90                  95  
  
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
       100                 105                 110  
  
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
       115                 120                 125  
  
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
       130                 135                 140  
  
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
       145                 150                 155                 160  
  
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
       165                 170                 175  
  
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
       180                 185                 190  
  
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
       195                 200                 205  
  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
       210                 215                 220  
  
 Glu Arg Cys Val Glu Ile Pro  
       225                 230  
  
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   20                  25                  30  
  
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
   35                  40                  45  
  
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
   50                  55                  60  
  
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 25

<211> 231

<212> PRT

<213> human

<400> 25

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Lys Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 26

<211> 231

<212> PRT

<213> human

<400> 26

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Gln Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 27

<211> 231

<212> PRT

<213> human

<400> 27

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Val Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn

145	150	155	160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile			
165	170	175	
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg			
180	185	190	
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val			
195	200	205	
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu			
210	215	220	
Glu Arg Cys Val Glu Ile Pro			
225	230		
<210> 28			
<211> 231			
<212> PRT			
<213> human			
<400> 28			
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu			
1	5	10	15
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln			
20	25	30	
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln			
35	40	45	
Pro Gly Arg Leu Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr			
50	55	60	
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly			
65	70	75	80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln			
85	90	95	
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser			
100	105	110	
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile			
115	120	125	
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val			
130	135	140	
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn			
145	150	155	160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile			
165	170	175	

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 29  
<211> 231  
<212> PRT  
<213> human

<400> 29  
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Ala Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 30  
<211> 231  
<212> PRT  
<213> human

<400> 30  
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Ile Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro

225

230

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 31  
gaattcgtcg acccaccatg cctaaggcatt gccttc

36

<210> 32  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 32  
tggaatctgc acacatctct cc

22

<210> 33  
<211> 199  
<212> PRT  
<213> human

<220>  
<221> VARIANT  
<222> (139)  
<223> Wherein "X" is a space inserted in the Blast alignment analysis.

<400> 33  
Lys Pro Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu  
1 5 10 15

Gln Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe  
20 25 30

Val Gln Tyr Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp  
35 40 45

Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser  
50 55 60

Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly  
65 70 75 80

Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu  
85 90 95

Thr Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser  
 100 105 110  
 Leu Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys  
 115 120 125  
 Glu Lys Asn Val Ser Ile Glu Asp Tyr Tyr Xaa Glu Leu Leu Tyr Arg  
 130 135 140  
 Val Phe Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu  
 145 150 155 160  
 Gly Ala His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser  
 165 170 175  
 Tyr Cys Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser  
 180 185 190  
 Gln Arg Ser Glu Glu Arg Cys  
 195

<210> 34  
 <211> 231  
 <212> PRT  
 <213> human

<400> 34  
 Ser Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu  
 1 5 10 15  
 Ser Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln  
 20 25 30  
 Lys Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln  
 35 40 45  
 Ala Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr  
 50 55 60  
 Lys Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly  
 65 70 75 80  
 Thr Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr  
 85 90 95  
 Glu Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser  
 100 105 110  
 Ala Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu  
 115 120 125  
 Asp Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val  
 130 135 140  
 Leu Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn  
 145 150 155 160

Ala Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg  
180 185 190

Ala Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys  
210 215 220

Glu Arg Cys Val Gln Ile Pro  
225 230

<210> 35

<211> 231

<212> PRT

<213> human

<400> 35

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg

180

185

190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
210 215 220

Glu Arg Cys Val Glu Ile Pro  
225 230

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR Primer

<400> 36

cttgcaacca ttagtgcctaa acattgc

27

<210> 37

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR Primer

<400> 37

atgatgccta aacattgctt tctagg

26

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR Primer

<400> 38

gaaactctgg ttgccagaca agcacac

27

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR Primer

<400> 39

caaggagaga tgtgtgcaga ttccatga

28